

Figure 1

1	CGGTGGCGCCCGTTCTAGAACTAGTGGATCCCCCGGGATGCAGGAATTCGGCAGCAGAGAAA	60
61	GTGCGGCGGAAAGTAAGAGGCTCACTGGGGAAGACTGCCGGGATCCAGGTCTCCGGGGTC	120
121	CGCTTTGGCCAGAGGCGCGGAAGGAAGCAGTGCCCGGCGACACTGCACCCATCCCGGCTG	180
181	CTTTTGCTGCGCCCTCTCAGCTTCCCAAGAAAGGCATCGTCATGTGATCATCACCTAAGA	240
241	ACTAGAACATCAGCAGGCCCTTAGAAGCCTCACTCTTGCCCTCCCTTTAATATCTCAAA	300
301	GGATGACACTTCTGTGGTGTGTAGTGAGTCTCTACTTTTATGGAATCCTGCAAAGTGATG	360
	<u>M T L L W C V V S L Y F Y G I L O S D A</u>	
361	CCTCAGAACGCTGCGATGACTGGGGACTAGACACCATGAGGCAAATCCAAGTGTTTGAAG	420
	S E R C D D W G L D T M R Q I Q V F E D	
421	ATGAGCCAGCTCGCATCAAGTGCCCACTCTTTGAACACTTCTTGAAATTCAACTACAGCA	480
	E P A R I K C P L F E H F L K F N Y S T	
481	CAGCCCATTCAGCTGGCCTTACTCTGATCTGGTATTGGAATAAGCAGGACCGGGACCTTG	540
	A H S A G L T L I W Y W T K Q D R D L E	
541	AGGAGCCAATTAACCTCCGCCTCCCCGAGAACCGCATAGTAAGGAGAAAGATGTGCTGT	600
	E P I N F R L P E N R I S K E K D V L W	
601	GGTTCGGGCCCACTCTCCTCAATGACACTGGCAACTATACCTGCATGTTAAGGAACACTA	660
	F R P T L L N D T G N Y T C M L R N T T	
661	CATATTGCAGCAAAGTTGCATTTCCCTTGGAAGTTGTTCAAAAAGACAGCTGTTTCAATT	720
	Y C S K V A F P L E V V Q K D S C F N S	
721	CCCCCATGAAACTCCAGTGACATAAAGTATAGTAATGATGATGATGATGATGATGATGAT	780
	P M K L P V H K L Y I E Y G I Q R I T C	
781	GTCCAAATGTAGATGGATATTTTCTTCCAGTGTCAAACCGACTATCACTTGGTATATGG	840
	P N V D G Y F P S S V K P T I T W Y M G	
841	GCTGTTTATAAATACAGAATTTTAATAATGTAATACCCGAAGGTATGAACTTGAGTTTCC	900
	C Y K I Q N F N N V I P E G M N L S F L	
901	TCATTGCCCTTAATTTCAAATAATGAAATTAACATGTGTTGTTACATATCCAGAAAATG	960
	I A L I S N N G N Y T C V V T Y P E N G	
961	GACGTACGTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAATG	1020
	R T F H L T R T L T V K V V G S P K N A	
1021	CAGTGCCCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACAGGAG	1080
	V P P V I H S P N D H V V Y E K E P G E	
1081	AGGAGCTACTCATTCCTGTACGGTCTATTTTAGTTTCTGATGGATTCTCGCAATGAGG	1140
	E L L I P C T V Y F S F L M D S R N E V	
1141	TTTGGTGGACCATTTGATGGAAAAAACCTGATGACATCACTATTGATGTCACCATTAACG	1200
	W W T I D G K K P D D I T I D V T I N E	
1201	AAAGTATAAGTCATAGTAGAACAGAGATGAACTAGAACTCAGATTTTGAGCATCAAGA	1260
	S I S H S R T E D E T R T Q I L S I K K	
1261	AAGTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTAGTAGAAGTGCCAAAGGCG	1320
	V T S E D L K R S Y V C H A R S A K G E	
1321	AAGTTGCCAAAGCAGCCAAGGTGAAGCAGAAAGGTAATAGATGCGGTCAGTGATGAATCT	1380
	V A K A A K V K Q K G N R C G Q *	
1381	CTCAGCTCCAAATTAACATTTGTGGTGAATAAGGACAAAAGGAGAGATTGAGAACAAGAGA	1440
1441	GCTCCAGCACCTAGCCTGACGGCATCTAACCCTAGTAATGAATCAAACCTTAAATGAAAA	1500
1501	ATATGAAAGTTTTCATCTATGTAAGATACTCAAAATATTGTTTCTGATATTGTTAGTACC	1560
1561	GTAATGCCCAAATGTAGCTAAAAAAATCGACGTGAGTACAGTGAGACACAATTTTGTGTC	1620
1621	TGTACAATTATGAAAAATTAAAAACAAAGAAATATTCAAAGCTACCAAAGATAGAAAAA	1680
1681	ACTGGTAGAGCCACATATTGTTGGTGAATTATTAAGACCCTTTTAAAAATCATTTCATGGT	1740
1741	AGAGTTTAAAGAGTCATAAAAAAGATTGCATCATCTGACCTAAGACTTTTCGGAATTTTCC	1800
1801	TGAACAAATAACAGAAAGGGAATTATATACCTTTTAATATTATTAGAAGCATTATCTGTA	1860
1861	GTTGTAAAACATTATTAATAGCAGCCATCCAATTGTATGCAACTAATTAAGGTATTGAAT	1920
1921	GTTTATTTTCCAAAAATGCATAATTATAATATTATTTTAAACACTATGTATCAATATTTA	1980
1981	AGCAGGTTTATAATATACCAGCAGCCACAATTGCTATAAATGAAAATCATTTAAATTATGA	2040
2041	TTTTAAATGGTATACACATGATTTCTATGTTGATAGTACTATATTATTCTACAATAAATG	2100
2101	GAAATTATAAAGCCTTCTTGTGCAAGTGCTGCTCCTAAAAA	2155

Figure 2A

Query: 303 MTLWCVVSLYFYGILQSDASERCDDWGLDIMRQIQVFEDEPARIKCPLFEHFLK+NYST 482
M LLW ++SL FYGILQS ASERCDDWGLDIMRQIQVFEDEPARIKCPLFEHFLK+NYST
Sbjct: 1 MGLLWYLMSLSFYGILQSHASERCDDWGLDIMRQIQVFEDEPARIKCPLFEHFLK+NYST 60

Query: 483 AHSAGI/TLIWYWTQDRDLEEPINFRLPENRISKEKDVLFWRPTLLNDTGNYTCMLRNTT 662
AHS+GI/TLIWYWT+QDRDLEEPINFRLPENRISKEKDVLFWRPTLLNDTGNYTCMLRNTT
Sbjct: 61 AHSSGI/TLIWYWTQDRDLEEPINFRLPENRISKEKDVLFWRPTLLNDTGNYTCMLRNTT 120

Query: 663 YCSKVAFFLEVVOKDSCFNPMKLPVHKLYIEYGIQRITCPNVDGYFPSSVKPTTTWYMG 842
YCSKVAFFLEVVOKDSCFNS M+ PVHK+YIE+GI +ITCPNVDGYFPSSVKP++TWY G
Sbjct: 121 YCSKVAFFLEVVOKDSCFNAMRFPVHKMYIEHGIHKITCPNVDGYFPSSVKPSVIWYKG 180

Query: 843 CYKIQNFNNVIPEGMNLISNNGNYTCVVTYPENGRIFHL/TRLTVKVVGSPKNA 1022
C +I +F+NV+PEGMNLIS I L+SNNNGNYTCVVTYPENGR FHL/TRLTVKVVGSPK+A
Sbjct: 181 CTEIVDFHNVLPPEGMNLISFFIPLVSNNNGNYTCVVTYPENGRIFHL/TRLTVKVVGSPKDA 240

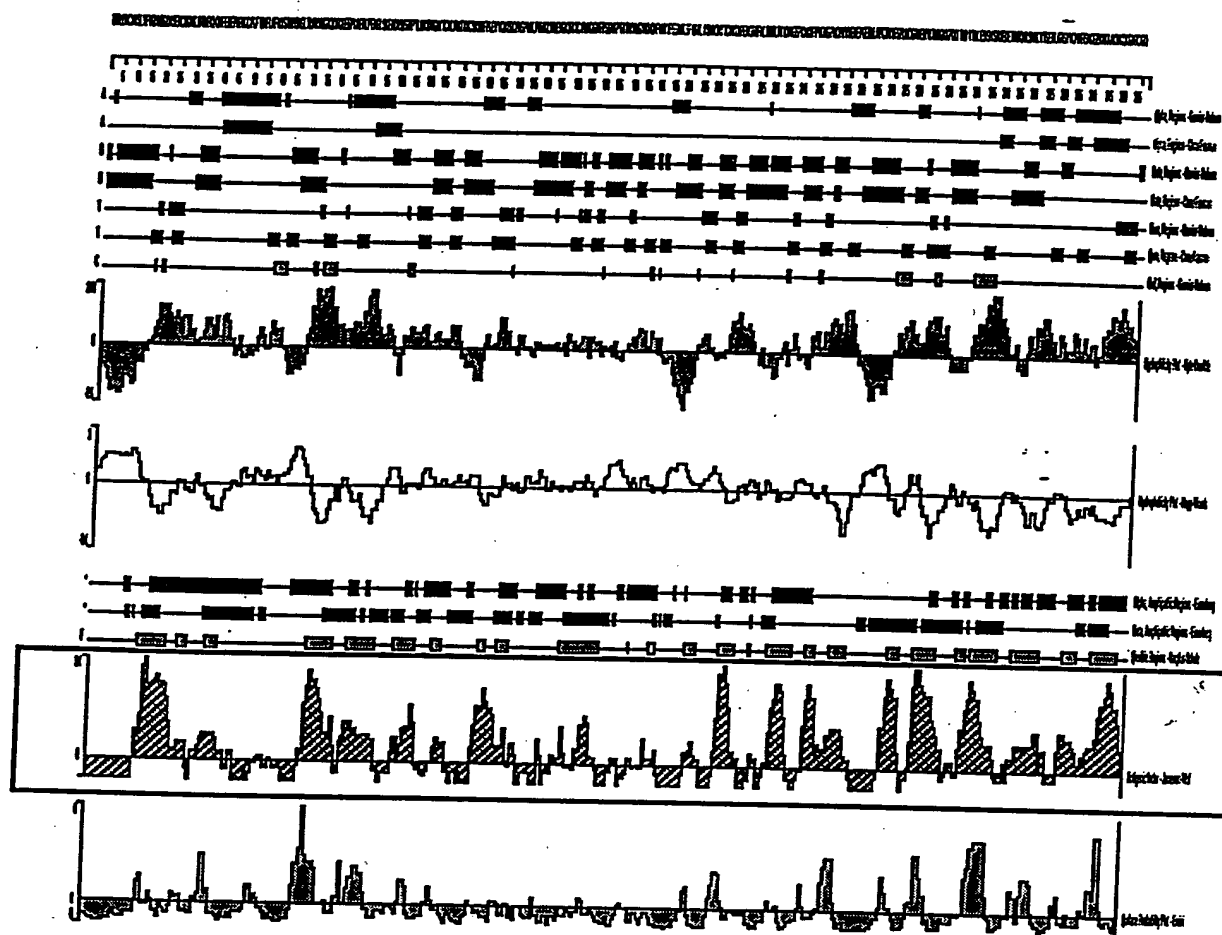
Query: 1023 VPPVIHSPNDHVVEKEPGEELLIPCVYFSFLMDSRNEVWWTIDGKKPDDITIDVTINE 1202
+PP I+SPND VVEKEPGEEL+IPC VYFSF+MDS NEVWWTIDGKKPDD+T+D+TINE
Sbjct: 241 LPPQIYSPNDRVVEKEPGEELVIPCKVYFSFIMDSHNEVWWTIDGKKPDDVTVDITINE 300

Query: 1203 SISHSRTEDETRTQILSIKKVTSSEDLKRSYVCHARSAKGEVAKAAKVQK 1352
S+S+S TEDETRTQILSIKKVT EDL+R+YVCHAR+ KGE +AAKVQK
Sbjct: 301 SVSYSSTEDETRTQILSIKKVTPEDLRRNYVCHARNTKGEAEQAAKVQK 350

Figure 2B

1 TCTATGAGAAAGAACCAGGAGAGGAGCTACTCATTCCCTGTACGGTCTAT 50
|||||
1060 TCTATGAGAAAGAACCAGGAGAGGAGCTACTCATTCCCTGTACGGTCTAT 1109
|||||
51 TTTAGTTTTCTGATGGATTCTCGCAATGAGGTTTGGTGGACCATTGATGG 100
|||||
1110 TTTAGTTTTCTGATGGATTCTCGCAATGAGGTTTGGTGGACCATTGATGG 1159
|||||
101 AAAAAACCTGATGACATCACTATTGATGTCACCATTAACGAAAGTATAA 150
|||||
1160 AAAAAACCTGATGACATCACTATTGATGTCACCATTAACGAAAGTATAA 1209
|||||
151 GTCATAGTAGAACAGAAGATGAAACAAGAACTCAGATTTTGAGCATCAAG 200
|||||
1210 GTCATAGTAGAACAGAAGATGAAACAAGAACTCAGATTTTGAGCATCAAG 1259
|||||
201 AAAGTTACCTCTGAGGATCTCAAGCGCANTANTGTCTGTCATGCTAGAAG 250
||||| : : |||||
1260 AAAGTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCATGCTAGAAG 1309
|||||
251 TGCCAAAGGCGAAGTTGCCAAAGCAGCCAAGGTGAAGCAGAAAG 294
|||||
1310 TGCCAAAGGCGAAGTTGCCAAAGCAGCCAAGGTGAAGCAGAAAG 1353
|||||

Figure 3



MTLLWCVVSLYFYGILQSDASERCDDWGLDTMRQIQVFEDEPARIKCPLFEHFL
KFNYSTAHSAGLTLIWYWTRQDRDLEEPINFRLPENRISKEKDVLWFRPTLLND
TGNYTCMLRNTTYCSKVAFPLEVVQKDSCFNSPMKLPVHKLYIEYGIQRITCPN
VDGYFPSSVKPTITWYMGCYKIQNFNNVIPEGMNLSFLIALISNNGNYTCVVTYP
ENGRTFHLTRTLTVKVGSPKNAVPPVIHSPNDHVVEKEPGEELLIPCTVYFSF
LMDSRNEVWWTIDGKKPDDITIDVTINESISHSRTEDETRTQILSIKKVTSEDLKR
SYVCHARSAKGEVAKAAKVQKGNRCGQ.